REMARKS

Applicants enclose herewith a signed "Power of Attorney by Assignee." Applicants also enclose herewith a copy of Form 1449 listing references that are of record in the present case based on the information disclosure statement filed in the parent application (from which the present application is a direct continuation).

Claims 1-28 are at issue in the present application and have been rejected by the Examiner. For clarity, the rejections at issue are set forth by number in the order they are herein addressed:

(1) Claims 1-28 are rejected under 35 U.S.C. §112, second paragraph as allegedly being indefinite or incomplete; and

(2) Claims 1-28 are rejected under the doctrine of obviousness-type double patenting in view of other patent or applications owned by the present assignee.

Applicants believe the present amendments and following remarks traverse the Examiner's rejection of the Claims.

Applicants note that all amendments and canceling of Claims presented herein are made without acquiescing to any of the Examiner's arguments or rejections, and solely for the purpose of expediting the patent application process in a manner consistent with the PTO's Patent Business Goals (PBG),[1] and without waiving the right to prosecute the amended or canceled Claims (or similar Claims) in the future.

1. Claims 1-28 35 U.S.C. §112 Rejections

Claims 1-15 stand rejected under 35 U.S.C. §112, second paragraph, for allegedly lacking antecedent basis in the preamble of Claim 1. In particular, the Examiner asserts "[t]he preamble to Claim 1 recites the function 'a method for determination of structure,' but the method steps result in detection and quantification of the probe/folded DNA complex and not the determination of the structure of the target DNA sequence." Office Action, pg. 3. The Applicants respectfully disagree. However, in order to expedite the prosecution process, the applicants have amended Claim 1 to link the preamble to the methods steps. This amendment renders the indefiniteness rejection moot, and the Applicants request that the rejection be withdrawn.

Claims 16-20 stand rejected under 35 U.S.C. §112, second paragraph, for allegedly lacking antecedent basis in the preamble of Claim 16. In particular, the Examiner asserts "the

[1] 65 Fed. Reg. 54603 (Sept. 8, 2000).

preamble of Claim 16 recites the function 'a method for analyzing the structure of nucleic acid targets,' but the method steps result in immobilization of the probe/folded DNA complex and not analysis of the structure of the target DNA sequence." Office Action, pg. 3. The Applicants respectfully disagree. However, in order to expedite the prosecution process, the Applicants have amended Claim 16 to link the preamble to the method steps. This amendment renders the indefiniteness rejection moot, and the Applicants request that the rejection be withdrawn.

Claims 21-28 stand rejected under 35 U.S.C. §112, second paragraph, for allegedly lacking antecedent basis in the preamble of Claim 21. In particular, the Examiner asserts "the preamble of Claim 21 recites the function 'a method for analyzing folded nucleic acid targets,' but the method steps result in immobilization of the probe/folded DNA complex and not analysis of the target DNA sequence." Office Action, pg. 3. The Applicants respectfully disagree. However, in order to expedite the prosecution process, the applicants have amended Claim 21 to link the preamble to the method steps. This amendment renders the indefiniteness rejection moot, and the Applicants request that the rejection be withdrawn.

Claims 16(a)(iv) and 21 (a)(iii) stand rejected under 35 U.S.C. §112, second paragraph. In particular, the Examiner asserts "the term 'testing zones' in claim 16(a)(iv) and claim 21(a)(iii) is *non sequitur* to the claim as a whole and has no recited relationship to the previoius steps of the corresponding claims." Office Action, pg. 3. The Applicants respectfully disagree. However, in order to expedite the prosecution process, the applicants have amended Claims 16 and 21 to remove the contested term. This amendment renders the indefiniteness rejection moot, and the Applicants request that the rejection be withdrawn.

Claims 17 and 24 stand rejected under 35 U.S.C. §112, second paragraph, for allegedly including indefinite terms. The Applicants respectfully disagree. However, in order to expedite the prosecution process, the Applicants now cancel Claims 17 and 24. This amendment renders the indefiniteness rejection moot.

Having addressed all of the 35 U.S.C. §112, second paragraph, rejections with appropriate claim amendments and cancellations, the Applicants request that such rejections be withdrawn.

2. Claims 1-28 Obviousness-Type Double Patenting Rejections

Claims 1-15 stand rejected as allegedly violating the judicially created doctrine of obviousness-type double patenting as being unpatentable over Claim 1 of U.S. Patent No. 6,214,545 (hereinafter '545) in view of USPN 6, 355,437 (hereinafter '437). The Applicants respectfully disagree and assert that the '437 patent does not constitute prior art to the present invention. The present invention has a priority date of September 19, 1997. The filing date for

the '437 patent was March 3, 1998. As such, the obviousness-type double patenting rejection is improper. The Examiner has also rejected claims as allegedly violating the judicially created doctrine of obviousness-type double patenting as being unpatentable over of USPN 6,210,880 (hereinafter '880), the parent case of the present application and has rejected claims in view of the '437 patent and the '880 patent in combination with co-pending Application No. 09/676,768. In order to expedite the prosecution of the present application, applicants submit herewith a Terminal Disclaimer that links the term of the present application to that of the '880 and '437 patents. In view of the Terminal Disclaimer, Applicants believe that the rejection should be withdrawn.

CONCLUSION

All grounds of rejection of the Office Action of May 23, 2002 having been addressed, it is respectfully submitted that the invention as claimed fully meets all requirements and that the claims should be passed to allowance.

Dated: November 22, 2002

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Appendix I

Version with markings to show changes made

Please cancel Claim 3, 17, and 24.
Please amend the following Claims.

1. (AMENDED) A method for identifying the presence of a nucleic acid target in a sample by determination of structure formation with said [in] nucleic acid target[s], comprising the steps of:
   a) providing:
      i) a sample suspected of having a folded target having a deoxyribonucleic acid sequence comprising one or more double stranded regions, and one or more single stranded regions, and further comprising two or more non-contiguous portions, and one or more intervening regions; and
      ii) one or more bridging oligonucleotide probes complementary to said two or more non-contiguous portions of said folded target; and
   b) mixing said folded target and said one or more probes under conditions such that said probe hybridizes to said folded target to form a probe/folded target complex; and[.]
   c) detecting said probe/folded target complex, thereby detecting the presence of said folded target in said sample.

16. (AMENDED) A method for comparing [analyzing] the structure of nucleic acid targets, comprising:
   a) providing:
      i) a first folded target having a nucleic acid sequence comprising first and second portions, said first and second portions each comprising one or more double stranded regions and one or more single stranded regions;
      ii) a second folded target having a nucleic acid sequence comprising a first portion that is identical to said first portion of said first folded target and a second portion that differs from said second portion of said first folded target because of a variation in nucleic acid sequence relative to said first folded target, said first and second portions each comprising one or more double stranded regions and

one or more single stranded regions;

iii) first and second bridging oligonucleotides said first bridging oligonucleotide complementary to said first portion of said first and second folded targets and said second bridging oligonucleotide complementary to said second portion of said first and second folded targets; and

[iv) a solid support comprising first, second, third and fourth testing zones, each zone capable of capturing and immobilizing said first and second bridging oligonucleotides;]

b) contacting said first folded target with said first bridging oligonucleotide under conditions such that said first bridging oligonucleotide binds to said first folded target to form a probe/folded target complex in a first mixture;

c) contacting said first folded target with said second bridging oligonucleotide under conditions such that said second bridging oligonucleotide binds to said first folded target to form a probe/folded target complex in a second mixture;

d) contacting said second folded target with said first bridging oligonucleotide to form a third mixture;

e) contacting said second folded target with said second bridging oligonucleotide to form fourth mixture; and

[f) adding said first, second, third and fourth mixtures to said first, second, third and fourth testing zones of said solid support, respectively, under conditions such that said first and second bridging oligonucleotides are captured and immobilized.]

f) <u>comparing the amount of probe/folded target complex in said first, second, third, and fouth mixtures.</u>

21. (AMENDED) A method for analyzing folded nucleic acid targets, comprising:

a) providing:

i) a first folded target having a nucleic acid sequence comprising first and second portions, wherein said first and second portions each comprise one or more double stranded regions and one or more single stranded regions;

ii) a second folded target having a nucleic acid sequence comprising a first portion that is identical to said first portion of said first folded

target, and a second portion that differs from said second portion of said first folded target because of a variation in nucleic acid sequence relative to said first folded target, said first and second portions each comprising one or more double stranded regions and one or more single stranded regions;

iii) a solid support comprising [first and second testing zones, each of said zones] comprising immobilized first and second bridging oligonucleotides, said first bridging oligonucleotide complementary to said first portion of said first and second folded targets and second bridging oligonucleotide complementary to said second portion of said first and second folded targets; and

b) contacting said first and second folded targets with said solid support under conditions such that said first and second bridging oligonucleotides hybridize to said first folded target to form a probe/folded target complex; and [.]

c) analyzing the amount of probe/folded target complex formed on said solid support at said first and second testing zones.

Appendix II

Pending Claims

1. (AMENDED) A method for identifying the presence of a nucleic acid target in a sample by determination of structure formation with said nucleic acid target, comprising the steps of:
   a) providing:
      i) a sample suspected of having a folded target having a deoxyribonucleic acid sequence comprising one or more double stranded regions, and one or more single stranded regions, and further comprising two or more non-contiguous portions, and one or more intervening regions; and
      ii) one or more bridging oligonucleotide probes complementary to said two or more non-contiguous portions of said folded target; and
   b) mixing said folded target and said one or more probes under conditions such that said probe hybridizes to said folded target to form a probe/folded target complex; and
   c) detecting said probe/folded target complex, thereby detecting the presence of said folded target in said sample.

2. The folded target of Claim 1, wherein said one or more intervening regions comprises at least five nucleotides.

4. The method of Claim 1, further comprising quantitating the amount of probe/folded target complex formed.

5. The method of Claim 1, wherein said probe in said probe/folded target complex is hybridized to at least one single stranded region of said folded target.

6. The method of Claim 1, wherein said bridging oligonucleotide probe further comprises a moiety that permits the capture of said bridging oligonucleotide probe by a solid support.

7. The method of Claim 6, wherein said detecting the presence of said probe/folded target complex comprises exposing said probe/folded target complex to a solid

support under conditions such that said bridging oligonucleotide is captured by said solid support.

8. The method of Claim 7, wherein said moiety comprises a biotin moiety and said solid support comprises a surface having a compound capable of binding to said biotin moiety, said compound selected from the group consisting of avidin and streptavidin.

9. The method of Claim 1, wherein said folded target is labelled.

10. The method of Claim 1, wherein said folded target comprises a deoxyribonucleic acid sequence having a moiety that permits its capture by a solid support.

11. The method of Claim 10, wherein said detecting the presence of said probe/folded target complex comprises exposing said probe/folded target complex to a solid support under conditions such that said folded target is captured by said solid support.

12. The method of Claim 11, wherein said moiety comprises a biotin moiety and said solid support comprises a surface having a compound capable of binding to said biotin moiety, said compound selected from the group consisting of avidin and streptavidin.

13. The method of Claim 1, wherein said bridging oligonucleotide probe is labelled.

14. The method of Claim 1, wherein said bridging oligonucleotide probe is attached to a solid support.

15. The method of Claim 1, wherein said folded target nucleic acid is attached to a solid support.

16. (AMENDED) A method for comparing the structure of nucleic acid targets, comprising:

a) providing:

i) a first folded target having a nucleic acid sequence comprising first and second portions, said first and second portions each comprising one or more double stranded regions and one or more single stranded regions;

ii) a second folded target having a nucleic acid sequence comprising a first portion that is identical to said first portion of said first folded target and a second portion that differs from said second portion of said first folded target because of a variation in nucleic acid sequence relative to said first folded target, said first and second portions each comprising one or more double stranded regions and one or more single stranded regions;

iii) first and second bridging oligonucleotides said first bridging oligonucleotide complementary to said first portion of said first and second folded targets and said second bridging oligonucleotide complementary to said second portion of said first and second folded targets; and

b) contacting said first folded target with said first bridging oligonucleotide under conditions such that said first bridging oligonucleotide binds to said first folded target to form a probe/folded target complex in a first mixture;

c) contacting said first folded target with said second bridging oligonucleotide under conditions such that said second bridging oligonucleotide binds to said first folded target to form a probe/folded target complex in a second mixture;

d) contacting said second folded target with said first bridging oligonucleotide to form a third mixture;

e) contacting said second folded target with said second bridging oligonucleotide to form fourth mixture; and

f) comparing the amount of probe/folded target complex in said first, second, third, and fouth mixtures.

18. The method of Claim 16, wherein the hybridization of said first bridging oligonucleotide in step d) to said second folded target is reduced relative to the hybridization of said first bridging oligonucleotide in step c) to said first folded target.

19. The method of Claim 16, wherein said first and second targets comprise DNA.

20. The method of Claim 16, wherein said first and second bridging oligonucleotides comprise DNA.

21. (AMENDED) A method for analyzing folded nucleic acid targets, comprising:
    a) providing:
        i) a first folded target having a nucleic acid sequence comprising first and second portions, wherein said first and second portions each comprise one or more double stranded regions and one or more single stranded regions;
        ii) a second folded target having a nucleic acid sequence comprising a first portion that is identical to said first portion of said first folded target, and a second portion that differs from said second portion of said first folded target because of a variation in nucleic acid sequence relative to said first folded target, said first and second portions each comprising one or more double stranded regions and one or more single stranded regions;
        iii) a solid support comprising comprising immobilized first and second bridging oligonucleotides, said first bridging oligonucleotide complementary to said first portion of said first and second folded targets and second bridging oligonucleotide complementary to said second portion of said first and second folded targets; and
    b) contacting said first and second folded targets with said solid support under conditions such that said first and second bridging oligonucleotides hybridize to said first folded target to form a probe/folded target complex; and

c) analyzing the amount of probe/folded target complex formed on said solid support at said first and second testing zones.

22. The method of Claim 21, wherein said contacting of step b) comprises adding said first folded target to said first testing zone and adding said second folded target to said second testing zone.

23. The method of Claim 21, wherein said first and second bridging oligonucleotides are immobilized in separate portions of said testing zones.

25. The method of Claim 23, wherein said first bridging oligonucleotide in said second testing zone hybridizes to said second folded target with a reduced efficiency compared to the hybridization of said first bridging oligonucleotide in first testing zone to said first folded target.

26. The method of Claim 21, wherein said first and second folded targets comprise DNA.

27. The method of Claim 21, wherein said first and second folded targets comprise RNA.

28. The method of Claim 21, wherein said first and second bridging oligonucleotides comprise DNA.